

SEQUENCE LISTING



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TECH CENTER 1600/2300

(1) GENERAL INFORMATION:

- (i) APPLICANT: Lu, Kuang-hui
Pang, Kevin
- (ii) TITLE OF INVENTION: Methods and Reagents for Treating
Glucose Metabolic Disorders
- (iii) NUMBER OF SEQUENCES: 3
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Foley, Hoag & Eliot
(B) STREET: One Post Office Square
(C) CITY: Boston
(D) STATE: MA
(E) COUNTRY: USA
(F) ZIP: 02109
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: ASCII (text)
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE: 10-FEB-2000
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Vincent, Matthew P.
(B) REGISTRATION NUMBER: 36,709
(C) REFERENCE/DOCKET NUMBER: ONV-058.01
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (617) 832-1000
(B) TELEFAX: (617) 832-7000

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Tyr Pro Ile Lys Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu
1 5 10 15

Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr
20 25 30

Arg Gln Arg Tyr
35

(3) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 582 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 81..371

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 81..164

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 165..371

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CAGCTTGACC TGCGGCAGTG CAGCCCTTGG GACTTCCCTC GCCTTCCACC TCCTGCTCGT 60
CTGCTTCACA AGCTATCGCT ATG GTG TTC GTG CGC AGG CCG TGG CCC GCC 110
Met Val Phe Val Arg Arg Pro Trp Pro Ala
-28 -25 -20
TTG ACC ACA GTG CTT CTG GCC CTG CTC GTC TGC CTA GGG GCG CTG GTC 158
Leu Thr Thr Val Leu Leu Ala Leu Leu Val Cys Leu Gly Ala Leu Val
-15 -10 -5
GAC GCC TAC CCC ATC AAA CCC GAC GCT CCC GGC GAA GAC GCC TCG CCG 206
Asp Ala Tyr Pro Ile Lys Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro
1 5 10
GAG GAG CTG AAC CGC TAC TAC GCC TCC CTG CGC CAC TAC CTC AAC CTG 254
Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu
15 20 25 30
GTC ACC CGG CAG CGG TAT GGG AAA AGA GAC GGC CCG GAC AGG CTT CTT 302
Val Thr Arg Gln Arg Tyr Gly Lys Arg Asp Gly Pro Asp Arg Leu Leu
35 40 45
TCC AAA ACG TTC TTC CCC GAC GGC GAG GAC CGC CCC GTC AGG TCG CGG 350
Ser Lys Thr Phe Phe Pro Asp Gly Glu Asp Arg Pro Val Arg Ser Arg
50 55 60

TCG GAG GGC CCA GAC CTG TGG TGAGGACCCC TGAGGCCTCC TGGGAGATCT 401
Ser Glu Gly Pro Asp Leu Trp
65

GCCAACCACG CCCACGTCAT TTGCATACGC ACTCCCGACC CCAGAAACCC GGATTCTGCC 461

TCCCGACGGC GCGTCTGGG CAGGGTTCGG GTGCGGCCCT CCGCCCGCGT CTCGGTGCCC 521

CCGCCCCCTG GGCTGGAGGG CTGTGTGTGG TCCTTCCTG GTCCCAAAAT AAAGAGCAAA 581

T 582

(4) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Val Phe Val Arg Arg Pro Trp Pro Ala Leu Thr Thr Val Leu Leu
-28 -25 -20 -15

Ala Leu Leu Val Cys Leu Gly Ala Leu Val Asp Ala Tyr Pro Ile Lys
-10 -5 1

Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg Tyr
5 10 15 20

Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
25 30 35

Gly Lys Arg Asp Gly Pro Asp Arg Leu Leu Ser Lys Thr Phe Phe Pro
40 45 50

Asp Gly Glu Asp Arg Pro Val Arg Ser Arg Ser Glu Gly Pro Asp Leu
55 60 65

Trp